Amendments to the Claims begin on page 3

Remarks begin on page 8

Amendments to the Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims

1. (currently amended) A method for determining whether a ~~of screening for~~ candidate agent~~s~~ is capable of modulating germline transcription, comprising:
   a) adding a ~~library of~~ candidate agent~~s~~ to a plurality of cells;
   b) preparing mRNA from said plurality of cells to form an mRNA mixture;
   c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP;
   d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and
   e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent~~; and~~ to thereby
   ~~f)~~ identify~~ing at least one~~ a candidate agent that alters the amount of said first germline mRNA.

2. (original) A method according to claim 1, further comprising stimulating said cells to produce germline mRNA.

3. (original) A method according to claim 1, wherein said RPP is labeled.

4. (original) A method according to claim 3, wherein said label is a fluorescent label.

5. (original) A method according to claim 3, wherein said label is a radioisotope.

6. (original) A method according to claim 1, wherein said germline mRNA is Ig alpha-1.

7. (original) A method according to claim 1, wherein said germline mRNA is Ig alpha-2.

8. (original) A method according to claim 1, wherein said germline mRNA is Ig epsilon.

9. (original) A method according to claim 1, wherein said germline mRNA is Ig gamma-1.

10. (original) A method according to claim 1, wherein said germline mRNA is Ig gamma-2.

11. (original) A method according to claim 1, wherein said germline mRNA is Ig gamma-3.

12. (original) A method according to claim 1, wherein said germline mRNA is Ig gamma-4.

13. (original) A method according to claim 1, wherein said RPP has a sequence selected from the group consisting of the sequences depicted in Figure 3.

14. (original) A method according to claim 1, wherein said RPP has a sequence selected from the group consisting of the sequences depicted in Figure 4.

15. (cancelled)

16. (cancelled)

17. (Currently amended) A method according to claim 1, further comprising:

a) adding to said mixture at least a second RNAse protection probe (RPP) substantially complementary to a second germline mRNA to form a second hybridization complex between said second germline mRNA and said second RPP;

b) quantifying the amount of said second germline mRNA as compared to a cell in the absence of a candidate agent~~; and~~ to thereby

~~c)~~ identify~~ing at least one~~ a candidate agent that alters the amount of said first germline mRNA but not said second germline mRNA.

18. (Currently amended) A method according to claim 1, wherein said ~~library comprises~~ candidate agent is a small molecules.

19. (Currently amended) A method according to claim 1, wherein said ~~library comprises~~ candidate agent is a peptides.

20. (Currently amended) A method according to claim 19, wherein said peptides ~~are~~ is a random peptides.

21. (Currently amended) A method according to claim 19, wherein said peptides ~~are~~ is a partially random peptides.

22. (Currently amended) A method according to claim 19, wherein said adding is done using a retroviruses encoding said peptides.

23. (Currently amended) A method according to claim 19 wherein said adding is done using a retroviruses comprising sequence derived from a cDNA library.

24. (withdrawn) A method of quantifying the amount of a plurality of germline constructs comprising:

a) preparing mRNA from said plurality of cells to form an mRNA mixture;

c) adding at least three RNAse protection probes (RPPs) selected from the group consisting of the sequences depicted in Figures 3 and 4;

d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested;

e) quantifying the amount of said germline mRNA.

25. (withdrawn) A kit for quantifying the amount of germline mRNA in a sample, comprising

a) at least one RNAse protection probe (RPP) comprising a nucleic acid sequence selected from the group consisting of the nucleic acid sequences of the Igα1, Igα2, Ig-epsilon, Ig gamma-1, Ig gamma-2, Ig gamma-3 and Ig gamma-4 RPPs set forth in Figures 3 and 4; and

b) an RNAse protection enzyme (RPE);
and optionally comprising at least one RNAse protection probe (RPP) which is substantially complementary to a transcript of a housekeeping gene.

26. (withdrawn) A kit according to claim 25, wherein all RNAse protection probes are labeled.

27. (New) The method of claim 1, wherein said first RNAse protection probe (RPP) and said first germline mRNA contain less than 5 base mismatches.

28. (New) A method according to claim 6, wherein said RPP comprises the sequence set forth as SEQ ID NO:7.

29. (New) A method according to claim 7, wherein said RPP comprises the sequence set forth as SEQ ID NO:1 or 8.

30. (New) A method according to claim 8, wherein said RPP comprises the sequence set forth as SEQ ID NO:2 or 9.

31. (New) A method according to claim 9, wherein said RPP comprises the sequence set forth as SEQ ID NO:3 or 10.

32. (New) A method according to claim 10, wherein said RPP comprises the sequence set forth as SEQ ID NO:4 or 11.

33. (New) A method according to claim 11, wherein said RPP comprises the sequence set forth as SEQ ID NO:5 or 12.

34.(New) A method according to claim 12, wherein said RPP comprises the sequence set forth as SEQ ID NO:6 or 13.